SEQUENCE LISTING

<110> Meyers, Rachel A.

<120> 26583, A NOVEL SERINE/THREONINE
PHOSPHATASE AND USES THEREFOR

<130> 10448-025001

<150> US 60/187,454
<151> 2000-03-07

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 2838
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (462)...(2072)

<221> misc_feature
<222> (1)...(2838)
<223> n = A,T,C or G

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trygcssykw yamrakmymm rmkttkaaaa amcmrraaag ttaaytggta agtttagtct     120
ttttgtcttt tatttcaagg tcccggatcc ggtggtggtg caaatcaaag aactgctcct     180
cagtggatgt tgcctttact tctaggcctg tacggaagtg ttacttctgc tctaaaagct     240
gcggaattct aatacgactc actatatggga gtcgacccac gcgtccggtg ggcaggccgg     300
gggtgagggc tcgcgctccg ggagctgcac ggggctgcgt ggaaagagcg ccgagcggtg     360
gcgtcgttgt cgccccctcc tcgtcgggaa gaatcgtttg gtctcctgcc gtgcccggaa     420
tcccagtcag aagttccagc ctgccactgt tctctgatgc c atg cca gca cca act     476
                                              Met Pro Ala Pro Thr
                                                1               5

caa ctg ttt ttt cct ctc atc cgt aac tgt gaa ctg agc agg atc tat     524
Gln Leu Phe Phe Pro Leu Ile Arg Asn Cys Glu Leu Ser Arg Ile Tyr
             10              15              20

ggc act gca tgt tac tgc cac cac aaa cat ctc tgt tgt tcc tca tcg     572
Gly Thr Ala Cys Tyr Cys His His Lys His Leu Cys Cys Ser Ser Ser
             25              30              35

tac att cct cag agt cga ctg aga tac aca cct cat cca gca tat gct     620
Tyr Ile Pro Gln Ser Arg Leu Arg Tyr Thr Pro His Pro Ala Tyr Ala
             40              45              50

acc ttt tgc agg cca aag gag aac tgg tgg cag tac acc caa gga agg     668
Thr Phe Cys Arg Pro Lys Glu Asn Trp Trp Gln Tyr Thr Gln Gly Arg
     55              60              65

aga tat gct tcc aca cca cag aaa ttt tac ctc aca cct cca caa gtc     716
Arg Tyr Ala Ser Thr Pro Gln Lys Phe Tyr Leu Thr Pro Pro Gln Val
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                 70                      75                      80                      85

aat agc atc ctt aaa gct aat gaa tac agt ttc aaa gtg cca gaa ttt        764
Asn Ser Ile Leu Lys Ala Asn Glu Tyr Ser Phe Lys Val Pro Glu Phe
                90                      95                     100

gac ggc aaa aat gtc agt tct atc ctt gga ttt gac agc aat cag ctg        812
Asp Gly Lys Asn Val Ser Ser Ile Leu Gly Phe Asp Ser Asn Gln Leu
            105                     110                     115

cct gca aat gca ccc att gag gac cgg aga agt gca gca acc tgc ttg        860
Pro Ala Asn Ala Pro Ile Glu Asp Arg Arg Ser Ala Ala Thr Cys Leu
        120                     125                     130

cag acc aga ggg atg ctt ttg ggg gtt ttt gat ggc cat gca ggt tgt        908
Gln Thr Arg Gly Met Leu Leu Gly Val Phe Asp Gly His Ala Gly Cys
        135                     140                     145

gct tgt tcc cag gca gtc agt gaa aga ctc ttt tat tat att gct gtc        956
Ala Cys Ser Gln Ala Val Ser Glu Arg Leu Phe Tyr Tyr Ile Ala Val
150                     155                     160                     165

tct ttg tta ccc cat gag act ttg cta gag att gaa aat gca gtg gag       1004
Ser Leu Leu Pro His Glu Thr Leu Leu Glu Ile Glu Asn Ala Val Glu
                    170                     175                     180

agc ggc cgg gca ctg cta ccc att ctc cag tgg cac aag cac ccc aat       1052
Ser Gly Arg Ala Leu Leu Pro Ile Leu Gln Trp His Lys His Pro Asn
            185                     190                     195

gat tac ttt agt aag gag gca tcc aaa ttg tac ttt aac agc ttg agg       1100
Asp Tyr Phe Ser Lys Glu Ala Ser Lys Leu Tyr Phe Asn Ser Leu Arg
            200                     205                     210

act tac tgg caa gag ctt ata gac ctc aac act ggt gag tcg act gat       1148
Thr Tyr Trp Gln Glu Leu Ile Asp Leu Asn Thr Gly Glu Ser Thr Asp
            215                     220                     225

att gat gtt aag gag gct cta att aat gcc ttc aag agg ctt gat aat       1196
Ile Asp Val Lys Glu Ala Leu Ile Asn Ala Phe Lys Arg Leu Asp Asn
230                     235                     240                     245

gac atc tcc ttg gag gcg caa gtt ggt gat cct aat tct ttt ctc aac       1244
Asp Ile Ser Leu Glu Ala Gln Val Gly Asp Pro Asn Ser Phe Leu Asn
                    250                     255                     260

tac ctg gtg ctt cga gtg gca ttt tct gga gcc act gct tgt gtg gcc       1292
Tyr Leu Val Leu Arg Val Ala Phe Ser Gly Ala Thr Ala Cys Val Ala
                265                     270                     275

cat gtg gat ggt gtt gac ctt cat gtg gcc aat act ggc gat agc aga       1340
His Val Asp Gly Val Asp Leu His Val Ala Asn Thr Gly Asp Ser Arg
            280                     285                     290

gcc atg ctg ggt gtg cag gaa gag gac ggc tca tgg tca gca gtc acg       1388
Ala Met Leu Gly Val Gln Glu Glu Asp Gly Ser Trp Ser Ala Val Thr
295                     300                     305

ctg tct aat gac cac aat gct caa aat gaa aga gaa cta gaa cgg ctg       1436
Leu Ser Asn Asp His Asn Ala Gln Asn Glu Arg Glu Leu Glu Arg Leu
310                     315                     320                     325
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aaa ttg gaa cat cca aag agt gag gcc aag agt gtc gtg aaa cag gat    1484
Lys Leu Glu His Pro Lys Ser Glu Ala Lys Ser Val Val Lys Gln Asp
                330                 335                 340

cgg ctg ctt ggc ttg ctg atg cca ttt agg gca ttt gga gat gta aag    1532
Arg Leu Leu Gly Leu Leu Met Pro Phe Arg Ala Phe Gly Asp Val Lys
                345                 350                 355

ttc aaa tgg agc att gac ctt caa aag aga gtg ata gaa tct ggc cca    1580
Phe Lys Trp Ser Ile Asp Leu Gln Lys Arg Val Ile Glu Ser Gly Pro
                360                 365                 370

gac cag ttg aat gac aat gaa tat acc aag ttt att cct cct aat tat    1628
Asp Gln Leu Asn Asp Asn Glu Tyr Thr Lys Phe Ile Pro Pro Asn Tyr
                375                 380                 385

cac aca cct cct tat ctc act gct gag cca gag gta act tac cac cga    1676
His Thr Pro Pro Tyr Leu Thr Ala Glu Pro Glu Val Thr Tyr His Arg
390                 395                 400                 405

tta agg cca cag gat aag ttt ctg gtg ttg gct act gat ggg ttg tgg    1724
Leu Arg Pro Gln Asp Lys Phe Leu Val Leu Ala Thr Asp Gly Leu Trp
                410                 415                 420

gag act atg cat agg cag gat gtg gtt agg att gtg ggt gag tac cta    1772
Glu Thr Met His Arg Gln Asp Val Val Arg Ile Val Gly Glu Tyr Leu
                425                 430                 435

act ggc atg cat cac caa cag cca ata gct gtt ggt ggc tac aag gtg    1820
Thr Gly Met His His Gln Gln Pro Ile Ala Val Gly Gly Tyr Lys Val
                440                 445                 450

act ctg gga cag atg cat ggc ctt tta aca gaa agg aga acc aaa atg    1868
Thr Leu Gly Gln Met His Gly Leu Leu Thr Glu Arg Arg Thr Lys Met
                455                 460                 465

tcc tcg gta ttt gag gat cag aac gca gca acc cat ctc att cgc cac    1916
Ser Ser Val Phe Glu Asp Gln Asn Ala Ala Thr His Leu Ile Arg His
470                 475                 480                 485

gct gtg ggc aac aac gag ttt ggg act gtt gat cat gag cgc ctc tct    1964
Ala Val Gly Asn Asn Glu Phe Gly Thr Val Asp His Glu Arg Leu Ser
                490                 495                 500

aaa atg ctt agt ctt cct gaa gag ctt gct cga atg tac aga gat gac    2012
Lys Met Leu Ser Leu Pro Glu Glu Leu Ala Arg Met Tyr Arg Asp Asp
                505                 510                 515

att aca atc att gta gtt cag ttc aat tct cat gtt gta ggg gcg tat    2060
Ile Thr Ile Ile Val Val Gln Phe Asn Ser His Val Val Gly Ala Tyr
                520                 525                 530

caa aac caa gaa tagtgagtgg ctctttcact ggcaattctc aaatgatata    2112
Gln Asn Gln Glu
                535

catttaaagg gcagattttt taaaaagata ctactataat aaacatttcc agttggtcat    2172
tctaagcatt tacccttttg atactctagc tagtcaggta ctccaaattg actttgcagc    2232
agggtggcag ggtcaggaga gtctggtcct gcctagctca gatttcatgg cacctgcact    2292
tgaagcaagt cacttcttta tcacaggtgt cttgaaacat tagcttcttt taccaacctg    2352
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agaaaattag gatgacctgg caaataagat cttgaatagg ccaaaagcaa gtatcttgct    2412
gtgtgtagtc tcttggttaa agtgaagaaa cagtactgtt cacacctttc ttcactgaga    2472
ttccagtgta catgagaaca tatatttatt ksmwkrwttt yywrrtacac agtctatgca    2532
ttwttcataw wmawttattt twgcctaaat aargtkkttw wcamatcyag tthwtcmatc    2592
matraacras mamcaascaa tctrtatktr tttttktkwk trwttrwytg rmakgmwtsy    2652
twaktrrrak ramtawmcwc mstyatccay ccgmyykmyt wmykwaaktr attgaaatat    2712
ttttwtttt gcccccccct tggagtcaag aagggttttt agttttatct tctyttctat    2772
tgaagttaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaag     2832
ggcgaa                                                               2838
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<210> 2
<211> 537
<212> PRT
<213> Homo sapiens

<400> 2
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Met Pro Ala Pro Thr Gln Leu Phe Phe Pro Leu Ile Arg Asn Cys Glu
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Leu Ser Arg Ile Tyr Gly Thr Ala Cys Tyr Cys His His Lys His Leu
                20                  25                  30
Cys Cys Ser Ser Ser Tyr Ile Pro Gln Ser Arg Leu Arg Tyr Thr Pro
            35                  40                  45
His Pro Ala Tyr Ala Thr Phe Cys Arg Pro Lys Glu Asn Trp Trp Gln
        50                  55                  60
Tyr Thr Gln Gly Arg Arg Tyr Ala Ser Thr Pro Gln Lys Phe Tyr Leu
65                  70                  75                  80
Thr Pro Pro Gln Val Asn Ser Ile Leu Lys Ala Asn Glu Tyr Ser Phe
                85                  90                  95
Lys Val Pro Glu Phe Asp Gly Lys Asn Val Ser Ser Ile Leu Gly Phe
            100                 105                 110
Asp Ser Asn Gln Leu Pro Ala Asn Ala Pro Ile Glu Asp Arg Arg Ser
        115                 120                 125
Ala Ala Thr Cys Leu Gln Thr Arg Gly Met Leu Leu Gly Val Phe Asp
    130                 135                 140
Gly His Ala Gly Cys Ala Cys Ser Gln Ala Val Ser Glu Arg Leu Phe
145                 150                 155                 160
Tyr Tyr Ile Ala Val Ser Leu Leu Pro His Glu Thr Leu Leu Glu Ile
                165                 170                 175
Glu Asn Ala Val Glu Ser Gly Arg Ala Leu Leu Pro Ile Leu Gln Trp
            180                 185                 190
His Lys His Pro Asn Asp Tyr Phe Ser Lys Glu Ala Ser Lys Leu Tyr
        195                 200                 205
Phe Asn Ser Leu Arg Thr Tyr Trp Gln Glu Leu Ile Asp Leu Asn Thr
    210                 215                 220
Gly Glu Ser Thr Asp Ile Asp Val Lys Glu Ala Leu Ile Asn Ala Phe
225                 230                 235                 240
Lys Arg Leu Asp Asn Asp Ile Ser Leu Glu Ala Gln Val Gly Asp Pro
                245                 250                 255
Asn Ser Phe Leu Asn Tyr Leu Val Leu Arg Val Ala Phe Ser Gly Ala
            260                 265                 270
Thr Ala Cys Val Ala His Val Asp Gly Val Asp Leu His Val Ala Asn
    275                 280                 285
Thr Gly Asp Ser Arg Ala Met Leu Gly Val Gln Glu Glu Asp Gly Ser
    290                 295                 300
Trp Ser Ala Val Thr Leu Ser Asn Asp His Asn Ala Gln Asn Glu Arg
305                 310                 315                 320
Glu Leu Glu Arg Leu Lys Leu Glu His Pro Lys Ser Glu Ala Lys Ser
                325                 330                 335
Val Val Lys Gln Asp Arg Leu Leu Gly Leu Leu Met Pro Phe Arg Ala
            340                 345                 350
Phe Gly Asp Val Lys Phe Lys Trp Ser Ile Asp Leu Gln Lys Arg Val
```

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                355                      360                      365
    Ile Glu Ser Gly Pro Asp Gln Leu Asn Asp Asn Glu Tyr Thr Lys Phe
                370                      375                      380
    Ile Pro Pro Asn Tyr His Thr Pro Pro Tyr Leu Thr Ala Glu Pro Glu
    385                      390                      395                      400
    Val Thr Tyr His Arg Leu Arg Pro Gln Asp Lys Phe Leu Val Leu Ala
                         405                      410                      415
    Thr Asp Gly Leu Trp Glu Thr Met His Arg Gln Asp Val Val Arg Ile
                         420                      425                      430
    Val Gly Glu Tyr Leu Thr Gly Met His His Gln Gln Pro Ile Ala Val
                435                      440                      445
    Gly Gly Tyr Lys Val Thr Leu Gly Gln Met His Gly Leu Leu Thr Glu
                450                      455                      460
    Arg Arg Thr Lys Met Ser Ser Val Phe Glu Asp Gln Asn Ala Ala Thr
    465                      470                      475                      480
    His Leu Ile Arg His Ala Val Gly Asn Asn Glu Phe Gly Thr Val Asp
                         485                      490                      495
    His Glu Arg Leu Ser Lys Met Leu Ser Leu Pro Glu Glu Leu Ala Arg
                         500                      505                      510
    Met Tyr Arg Asp Asp Ile Thr Ile Ile Val Val Gln Phe Asn Ser His
                         515                      520                      525
    Val Val Gly Ala Tyr Gln Asn Gln Glu
                530                      535
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<210> 3
<211> 1611
<212> DNA
<213> Homo sapiens

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cagagtcgac tgagatacac acctcatcca gcatatgcta ccttttgcag gccaaaggag       180
aactggtggc agtacaccca aggaaggaga tatgcttcca caccacagaa attttacctc       240
acacctccac aagtcaatag catccttaaa gctaatgaat acagtttcaa agtgccagaa       300
tttgacggca aaaatgtcag ttctatcctt ggatttgaca gcaatcagct gcctgcaaat       360
gcacccattg aggaccggag aagtgcagca acctgcttgc agaccagagg gatgcttttg       420
gggggttttttg atggccatgc aggttgtgct tgttcccagg cagtcagtga aagactcttt       480
tattatattg ctgtctcttt gttaccccat gagactttgc tagagattga aaatgcagtg       540
gagagcggcc gggcactgct acccattctc cagtggcaca agcaccccaa tgattacttt       600
agtaaggagg catccaaatt gtactttaac agcttgagga cttactggca agagcttata       660
gacctcaaca ctggtgagtc gactgatatt gatgttaagg aggctctaat taatgccttc       720
aagaggcttg ataatgacat ctccttggag gcgcaagttg gtgatcctaa ttcttttctc       780
aactacctgg tgcttcgagt ggcatttttct ggagccactg cttgtgtggc ccatgtggat       840
ggtgttgacc ttcatgtggc caatactggc gatagcagag ccatgctggg tgtgcaggaa       900
gaggacggct catggtcagc agtcacgctg tctaatgacc acaatgctca aaatgaaaga       960
gaactagaac ggctgaaatt ggaacatcca aagagtgagg ccaagagtgt cgtgaaacag      1020
gatcggctgc ttggcttgct gatgccattt agggcatttg gagatgtaaa gttcaaatgg      1080
agcattgacc ttcaaaagag agtgatagaa tctggcccag accagttgaa tgacaatgaa      1140
tataccaagt ttattcctcc taattatcac acacctcctt atctcactgc tgagccagag      1200
gtaacttacc accgattaag gccacaggat aagtttctgg tgttggctac tgatgggttg      1260
tgggagacta tgcataggca ggatgtggtt aggattgtgg gtgagtacct aactggcatg      1320
catcaccaac agccaatagc tgttggtggc tacaaggtga ctctgggaca gatgcatggc      1380
cttttaacag aaaggagaac caaaatgtcc tcggtatttg aggatcagaa cgcagcaacc      1440
catctcattc gccacgctgt gggcaacaac gagtttggga ctgttgatca tgagcgcctc      1500
tctaaaatgc ttagtcttcc tgaagagctt gctcgaatgt acagagatga cattacaatc      1560
attgtagttc agttcaattc tcatgttgta ggggcgtatc aaaaccaaga a               1611

<210> 4
<211> 300
<212> PRT
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<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 4
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Leu Asp Val Gly Val Ser Arg Met Gln Gly Trp Arg Lys Ser Met Glu
 1               5                  10                  15
Asp Ala His Ile Ala Leu Lys Asn Leu Asn Ser Ser Ser Ser Gly Lys
            20                  25                  30
Asp Ser Trp Ser Phe Phe Ala Val Phe Asp Gly His Gly Ser Gln Ala
            35                  40                  45
Ala Lys Tyr Ala Gly Lys His Leu His Lys Thr Ile Leu Ala Glu Arg
    50                  55                  60
Lys Ser Phe Pro Glu Gly Asp Pro Trp Glu Met Lys Leu Ser Asp Leu
65                  70                  75                  80
Glu Asp Ala Leu Lys Glu Ser Phe Leu Glu Ala Asp Thr Asp Glu Glu
                85                  90                  95
Leu Arg Ser Ala Glu Ala Ser Ala Ala Asn Lys Val Leu Thr Lys Glu
                100                 105                 110
Asp Leu Ser Ser Gly Ser Thr Ala Val Val Ala Leu Ile Arg Gly Asn
            115                 120                 125
Lys Leu Tyr Val Ala Asn Val Gly Asp Ser Arg Ala Val Leu Cys Arg
    130                 135                 140
Asn Gly Asn Ala Ile Lys Trp Ala Val Thr Leu Thr Glu Asp His Lys
145                 150                 155                 160
Pro Ser Asn Glu Asp Glu Arg Glu Arg Ile Glu Ala Ala Gly Gly Phe
                165                 170                 175
Val Ser Arg Val Ser Asn Gly Arg Val Asn Gly Val Leu Ala Val Ser
            180                 185                 190
Arg Ala Phe Gly Asp Phe Glu Leu Lys Pro Gly Ser Lys Leu Gly Pro
            195                 200                 205
Glu Glu Ser Leu Glu Ala Asn Tyr Glu Tyr Ile Lys Ser Pro Glu Gln
    210                 215                 220
Leu Val Thr Ala Glu Pro Asp Val Thr Ser Ser Thr Asp Leu Thr Pro
225                 230                 235                 240
Asp Lys Asp Glu Phe Leu Ile Leu Ala Cys Asp Gly Leu Trp Asp Val
                245                 250                 255
Val Ser Asp Gln Glu Val Val Asp Ile Val Arg Ser Glu Leu Ser Asp
            260                 265                 270
Gly Asn Lys Ser Ala Glu Asp Pro Met Glu Ala Ala Glu Lys Leu Val
    275                 280                 285
Asp Glu Ala Ile Ala Arg Gly Ser Glu Asp Asn Ile
    290                 295                 300
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<210> 5
<211> 338
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 5
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Glu Ser Ser Gly Lys Asn Leu Gly Leu Arg Tyr Gly Leu Gly Glu Ser
 1               5                  10                  15
Ser Met Gln Gly Trp Arg Lys Pro Met Glu Asp Ala His Val Ile Arg
            20                  25                  30
Pro Phe Phe Gly Val Phe Asp Gly His Gly Gly Ser Glu Ala Ala Lys
            35                  40                  45
Phe Leu Ser Lys Asn Leu His Glu Ile Leu Ala Glu Glu Leu Ser Phe
```

```
         50                        55                       60
Asp Lys Asp Glu Ser Leu Lys Glu Asn Glu Glu Leu Lys Asp Glu Pro
65                        70                       75                       80
Glu Ser Ser Glu Arg Leu Asn Gly Asp Lys Ser Leu Glu Asp Val Glu
                    85                       90                       95
Glu Ala Leu Arg Lys Ala Phe Leu Arg Thr Asp Glu Glu Ile Ser Thr
                   100                      105                      110
Ala Val Val Ala Leu Ile Arg Gly Asn Lys Leu Tyr Val Ala Asn Val
                   115                      120                      125
Gly Asp Ser Arg Ala Val Leu Cys Arg Asn Gly Lys Asp Ser Trp Glu
              130                      135                      140
Gly Val Arg Thr Tyr Ser Ala Val Gln Leu Thr Glu Asp His Lys Pro
145                      150                      155                      160
Ser Asn Glu Asp Glu Arg Glu Arg Ile Glu Ala Ala Gly Gly Glu Val
                   165                      170                      175
Glu Pro Ile Asp Arg Glu Phe Val Ser Asn Gly Gly Gly Val Val Trp
              180                      185                      190
Arg Val Asn Gly Val Val Ile Ser Leu Ala Val Ser Arg Ala Leu Gly
              195                      200                      205
Asp Phe Glu Leu Lys Lys Lys Glu Asp Glu Leu Ile Glu Glu Asn Arg
              210                      215                      220
Leu Tyr Glu Lys Phe Asp Pro Arg Leu Pro Gly Lys Glu Pro Tyr Val
225                      230                      235                      240
Ser Ala Glu Pro Glu Val Thr Val Val Glu Leu Ser Gln Thr Leu Val
                   245                      250                      255
Pro Thr Glu Asp Asp Asp Phe Leu Ile Leu Ala Ser Asp Gly Leu Trp
              260                      265                      270
Asp Val Leu Ser Asn Gln Glu Ala Val Asp Ile Val Arg Lys His Leu
              275                      280                      285
Arg Lys Gly Asp Asp Lys Glu Val Lys Ser Ala Ala Gln Glu Leu Ala
              290                      295                      300
Arg Ala Asp Ser Leu Arg Ser Lys Lys His Asn Asp Pro Lys Glu Ala
305                      310                      315                      320
Ala Lys Leu Leu Val Asp Leu Ala Leu Lys Asp Asn Ile Thr Val Val
              325                      330                      335
Val Val
```